

## Tables S9-18

**Table S9.** DEGs involved in cell wall metabolism in leaves of *C. grandis* seedlings exposed to Cu-toxicity

Accession No.	KEGG	Swiss-Prot	Log <sub>2</sub> (FC)
Plant-type cell wall (GO:0009505)			
Cg1g015520	LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	LRR receptor-like serine/threonine-protein kinase GSO2	-1.602
Cg4g008420	LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	Leucine-rich repeat extensin-like protein 4	-1.176
Cg2g024270	Interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]	Wall-associated receptor kinase-like 2	-1.330
Cg1g024330	Beta-galactosidase [EC:3.2.1.23]	Beta-galactosidase 10	-1.209
Cg3g014760	Nucleoporin SEH1	Protein EXORDIUM-like 2	-2.037
CgUng004910	Nucleoporin SEH1	Protein EXORDIUM-like 2	-2.760
Cg4g019830	Heparanase [EC:3.2.1.166]	Heparanase-like protein 3	-1.388
Cg5g008280	Saccharopepsin [EC:3.4.23.25]	Probable aspartyl protease At4g16563 {ECO:0000305}	-1.082
Cg7g011170	Alpha-mannosidase [EC:3.2.1.24]	Probable alpha-mannosidase At5g13980 {ECO:0000305}	-2.225
Cg7g014460	Alpha-D-xyloside xylohydrolase [EC:3.2.1.177]	Alpha-xylosidase 1	-1.159
Cg9g001580	Xylan 1,4-beta-xylosidase [EC:3.2.1.37]	Beta-D-xylosidase 1	-1.581
Cg5g038180	Xylan 1,4-beta-xylosidase [EC:3.2.1.37]	Probable beta-D-xylosidase 2	-1.672
Cg9g026970	O-palmitoleoyl-L-serine hydrolase [EC:3.1.1.98]	Pectin acetyltransferase 9 {ECO:0000303 PubMed:25115560}	-2.264
Cg9g002460	Sucrose synthase [EC:2.4.1.13]	Sucrose synthase 2	3.483
Cell wall organization (GO:0071555)			
Cg1g015500	LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	LRR receptor-like serine/threonine-protein kinase FLS2	-1.275
Cg1g015520	LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	LRR receptor-like serine/threonine-protein kinase GSO2	-1.602
Cg4g008420	LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	Leucine-rich repeat extensin-like protein 4	-1.176
Cg9g006130	LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	Leucine-rich repeat extensin-like protein 6	-2.603
Cg2g040340	Protein transport protein SEC61 subunit alpha	COBRA-like protein 10	-2.721
CgUng006010	Leucine-rich PPR motif-containing protein, mitochondrial	COBRA-like protein 1	9.115
Cg3g023440	Integrin-linked kinase-associated serine/threonine phosphatase 2C [EC:3.1.3.16]	Protein WALLS ARE THIN 1	2.919
Cg4g000800	Xyloglucan glycosyltransferase 4 [EC:2.4.1.-]	Probable xyloglucan glycosyltransferase 5	3.743
Cg1g007100	Xyloglucan:xyloglucosyl transferase [EC:2.4.1.207]	Probable xyloglucan endotransglucosylase/hydrolase protein 6	-1.880
Cg2g017560	Xyloglucan:xyloglucosyl transferase [EC:2.4.1.207]	Xyloglucan endotransglucosylase/hydrolase protein 9	-2.685
Cg2g020180	Omega-hydroxypalmitate O-feruloyl transferase [EC:2.3.1.188]	Omega-hydroxypalmitate O-feruloyl transferase	-3.290

Cg2g031930	F-box and leucine-rich repeat protein 2/20	Putative pectinesterase/pectinesterase inhibitor 22	-1.492
Cg1g013250	Pectinesterase [EC:3.1.1.11]	Pectinesterase 3	-2.176
Cg2g033370	Pectinesterase [EC:3.1.1.11]	Probable pectinesterase/pectinesterase inhibitor 6	-1.299
Cg4g018220	Pectinesterase [EC:3.1.1.11]	Probable pectinesterase/pectinesterase inhibitor 54	-2.108
Cg5g018160	Pectinesterase [EC:3.1.1.11]	Probable pectinesterase/pectinesterase inhibitor 61	-1.288
Cg9g026970	O-palmitoleoyl-L-serine hydrolase [EC:3.1.1.98]	Pectin acylesterase 9 {ECO:0000303 PubMed:25115560}	-2.264
Cg2g040360	Pectinesterase [EC:3.1.1.11]	Pectinesterase 2.2	1.647
Cg2g044240	DNA-directed RNA polymerase II subunit RPB1 [EC:2.7.7.6]	Glucan endo-1,3-beta-glucosidase 12	2.251
Cg8g014060	Glucan endo-1,3-beta-glucosidase 1/2/3 [EC:3.2.1.39]	Glucan endo-1,3-beta-glucosidase 14	1.055
Cg3g023860	Endoglucanase [EC:3.2.1.4]	Endoglucanase 10	1.121
Cg7g014460	Alpha-D-xyloside xylohydrolase [EC:3.2.1.177]	Alpha-xylosidase 1	-1.159
Cg5g009980	UDP-glucose 4-epimerase [EC:5.1.3.2]	Bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1	-1.862
Cg5g000440	Abhydrolase domain-containing protein 5 [EC:2.3.1.51]	Probable lysophospholipase BODYGUARD 3 {ECO:0000303 PubMed:16415209}	7.905
Cg6g008750	Abhydrolase domain-containing protein 5 [EC:2.3.1.51]	Probable lysophospholipase BODYGUARD 4 {ECO:0000303 PubMed:16415209}	2.244
Cg5g030310	Cytochrome P450 family 71 subfamily A	Cytochrome P450 83B1	3.608
Cg7g014840	Probable galacturonosyltransferase-like 1 [EC:2.4.1.-]	Probable galacturonosyltransferase-like 3	-1.814
Cg7g019950	N-hydroxythioamide S-beta-glucosyltransferase [EC:2.4.1.195]	UDP-glycosyltransferase 74B1	2.549
Cg7g021600	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	ARF guanine-nucleotide exchange factor GNOM	1.069
Cg9g007480	Cellulose synthase A [EC:2.4.1.12]	Cellulose synthase-like protein G2	1.063
Cell wall modification (GO:0042545)			
Cg1g015500	LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	LRR receptor-like serine/threonine-protein kinase FLS2	-1.275
Cg2g031930	F-box and leucine-rich repeat protein 2/20	Putative pectinesterase/pectinesterase inhibitor 22	-1.492
Cg1g013250	Pectinesterase [EC:3.1.1.11]	Pectinesterase 3	-2.176
Cg2g033370	Pectinesterase [EC:3.1.1.11]	Probable pectinesterase/pectinesterase inhibitor 6	-1.299
Cg4g018220	Pectinesterase [EC:3.1.1.11]	Probable pectinesterase/pectinesterase inhibitor 54	-2.108
Cg5g018160	Pectinesterase [EC:3.1.1.11]	Probable pectinesterase/pectinesterase inhibitor 61	-1.288
Cg2g040360	Pectinesterase [EC:3.1.1.11]	Pectinesterase 2.2	1.647

Cg5g030310	Cytochrome P450 family 71 subfamily A	Cytochrome P450 83B1	3.608
Cg7g019950	N-hydroxythioamide S-beta-glucosyltransferase [EC:2.4.1.195]	UDP-glycosyltransferase 74B1	2.549
Cell wall macromolecule metabolic process (GO:0044036)			
Cg1g000850	Basic endochitinase B [EC:3.2.1.14]	Basic endochitinase	-3.753
Cg8g000790	Basic endochitinase B [EC:3.2.1.14]	Endochitinase	-4.533
Cg8g000800	Basic endochitinase B [EC:3.2.1.14]	Endochitinase	-4.480
Cg5g026680	Chitinase [EC:3.2.1.14]	Chitinase 4	4.598
Cg1g007100	Xyloglucan:xyloglucosyl transferase [EC:2.4.1.207]	Probable xyloglucan endotransglucosylase/hydrolase protein 6	-1.880
Cg2g017560	Xyloglucan:xyloglucosyl transferase [EC:2.4.1.207]	Xyloglucan endotransglucosylase/hydrolase protein 9	-2.685
Cg2g020180	Omega-hydroxypalmitate O-feruloyl transferase [EC:2.3.1.188]	Omega-hydroxypalmitate O-feruloyl transferase	-3.290
Cg7g014460	Alpha-D-xyloside xylohydrolase [EC:3.2.1.177]	Alpha-xylosidase 1	-1.159
Cg5g039550	Mannan endo-1,4-beta-mannosidase [EC:3.2.1.78]	Mannan endo-1,4-beta-mannosidase 4	-1.919
Cg6g019480	Mannose-6-phosphate isomerase [EC:5.3.1.8]	Mannose-6-phosphate isomerase 1	1.247
Cell wall pectin biosynthetic process (GO:0052325)			
Cg2g020180	Omega-hydroxypalmitate O-feruloyl transferase [EC:2.3.1.188]	Omega-hydroxypalmitate O-feruloyl transferase	-3.290
Callose deposition in cell wall (GO:0052543)			
Cg1g015500	LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	LRR receptor-like serine/threonine-protein kinase FLS2	-1.275
Cg5g030310	Cytochrome P450 family 71 subfamily A	Cytochrome P450 83B1	3.608
Cg7g019950	N-hydroxythioamide S-beta-glucosyltransferase [EC:2.4.1.195]	UDP-glycosyltransferase 74B1	2.549
Cell wall thickening (GO:0052386)			
Cg1g015500	LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]	LRR receptor-like serine/threonine-protein kinase FLS2	-1.275
Cg5g030310	Cytochrome P450 family 71 subfamily A	Cytochrome P450 83B1	3.608
Cg7g019950	N-hydroxythioamide S-beta-glucosyltransferase [EC:2.4.1.195]	UDP-glycosyltransferase 74B1	2.549
Cell wall biogenesis (GO:0042546)			
Cg1g007100	Xyloglucan:xyloglucosyl transferase [EC:2.4.1.207]	Probable xyloglucan endotransglucosylase/hydrolase protein 6	-1.880
Cg2g017560	Xyloglucan:xyloglucosyl transferase [EC:2.4.1.207]	Xyloglucan endotransglucosylase/hydrolase protein 9	-2.685
Cg2g020180	Omega-hydroxypalmitate O-feruloyl transferase [EC:2.3.1.188]	Omega-hydroxypalmitate O-feruloyl transferase	-3.290
Cg2g040340	Protein transport protein SEC61 subunit alpha	COBRA-like protein 10	-2.721
Cg6g019480	Mannose-6-phosphate isomerase [EC:5.3.1.8]	Mannose-6-phosphate isomerase 1	1.247
Cg9g007480	Cellulose synthase A [EC:2.4.1.12]	Cellulose synthase-like protein G2	1.063
CgUng006010	Leucine-rich PPR motif-containing protein, mitochondrial	COBRA-like protein 1	9.115

Cg3g023440	Integrin-linked kinase-associated serine/threonine phosphatase 2C [EC:3.1.3.16]	Protein WALLS ARE THIN 1	2.919
Cg2g007490	Glucuronokinase [EC:2.7.1.43]	Glucuronokinase 1	1.774
Plant-type cell wall organization or biogenesis (GO:0071669)			
Cg2g020180	Omega-hydroxypalmitate O-feruloyl transferase [EC:2.3.1.188]	Omega-hydroxypalmitate O-feruloyl transferase	-3.290
Cg2g040340	Protein transport protein SEC61 subunit alpha	COBRA-like protein 10	-2.721
CgUng006010	Leucine-rich PPR motif-containing protein, mitochondrial	COBRA-like protein 1	9.115
Cg3g013250	Branched-chain amino acid aminotransferase [EC:2.6.1.42]	Branched-chain-amino-acid aminotransferase 2, chloroplastic	1.973
Cg3g023440	Integrin-linked kinase-associated serine/threonine phosphatase 2C [EC:3.1.3.16]	Protein WALLS ARE THIN 1	2.919
Cg9g007480	Cellulose synthase A [EC:2.4.1.12]	Cellulose synthase-like protein G2	1.063
Other			
Cg4g022640	Expansin	EG45-like domain containing protein 2	-4.198
Cg1g015970	Interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]	Wall-associated receptor kinase-like 10	2.024
Cg6g000930	Interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]   (RefSeq) putative wall-associated receptor kinase-like 16 (A)	Protein LYK5	6.121
Cg5g026300	Interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]	Wall-associated receptor kinase 5	-3.253

**Table S10.** DEGs related to stomata, chlorophyll and carotenoids metabolism, and photosynthesis in leaves of *C. grandis* seedlings exposed to Cu-toxicity

Accession No.	KEGG	Swiss-Prot	Log <sub>2</sub> (FC)
Stomatal opening (GO:1990069)			
Cg8g019250	RING finger and CHY zinc finger domain-containing protein 1 [EC:2.3.2.27]	E3 ubiquitin-protein ligase RZFP34 {ECO:0000305}	-2.350
Cg7g004470	Stomatal closure (GO:0090332) Heat shock 70kDa protein 1/2/6/8	Probable mediator of RNA polymerase II transcription subunit 37e	4.597
Chlorophyll biosynthetic process (GO:0015995)			
Cg2g021210	Protochlorophyllide reductase [EC:1.3.1.33]	Protochlorophyllide reductase, chloroplastic	-1.721
Cg5g028200	Magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase [EC:1.14.13.81]	Tetrapyrrole-binding protein, chloroplastic	-2.052
Cg6g017060		Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic	-1.080
Cg9g006330	Mitochondrial pyruvate carrier 2	Early light-induced protein 1, chloroplastic {ECO:0000305}	1.715
Chlorophyll catabolic process (GO:0015996)			
Cg5g009510	Magnesium dechelatase [EC:4.99.1.10]	Protein STAY-GREEN 1, chloroplastic	1.601
Cg5g020710	Chlorophyllase [EC:3.1.1.14]		2.019
Carotenoid biosynthetic process (GO:0016117)			
Cg6g018390	Geranylgeranyl diphosphate synthase, type II [EC:2.5.1.1 2.5.1.10 2.5.1.29]	Geranylgeranyl pyrophosphate synthase, chloroplastic	-1.239
Photosynthesis (ko00195)			
Cg9g013190	F-type H <sup>+</sup> -transporting ATPase subunit b	Putative ATP synthase protein YMF19	-1.145
Cg3g024680	Plastocyanin	Plastocyanin, chloroplastic	-1.448
Cg9g005290	Photosystem I subunit II	Photosystem I reaction center subunit II, chloroplastic	-1.501
Cg2g038220	Photosystem I subunit III	Photosystem I reaction center subunit III, chloroplastic	-1.014
Cg1g024920	Photosystem I subunit PsaN	Photosystem I reaction center subunit N, chloroplastic	-1.265
Cg7g005010	Photosystem II oxygen-evolving enhancer protein 2	PsbP-like protein 1, chloroplastic	-1.142
Cg7g012220	Photosystem II oxygen-evolving enhancer protein 2	Oxygen-evolving enhancer protein 2, chloroplastic	-1.749
Cg7g017970	Photosystem II PsbY protein	Photosystem II core complex proteins psbY, chloroplastic	-1.122
Cg2g040770	Photosystem II oxygen-evolving enhancer protein 3	Oxygen-evolving enhancer protein 3, chloroplastic	-2.463
Cg2g014580	Photosystem II Psb27 protein	Photosystem II repair protein PSB27-H1, chloroplastic	-1.149
Cg4g017260	Photosystem I subunit V	Photosystem I reaction center subunit V, chloroplastic	-1.799
Cg8g013250	Photosystem I subunit PsaO	Photosystem I subunit O	-2.645
Cg8g014070	Ferredoxin	Ferredoxin-3, chloroplastic	1.202
Photosynthesis- antenna proteins (ko00196)			
Cg7g006420	Light-harvesting complex I chlorophyll	Chlorophyll a-b binding protein 6A,	-1.626

Cg2g044430	a/b binding protein 1 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein 3C,	-1.333
Cg2g044450	a/b binding protein 1 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein 3C,	-1.625
Cg2g020050	a/b binding protein 1 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein 151,	-1.880
Cg2g021790	a/b binding protein 2 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein 13,	-1.361
Cg6g006850	a/b binding protein 3 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein CP29.2,	-1.890
Cg5g023620	a/b binding protein 4 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein CP26,	-1.740
Cg2g025410	a/b binding protein 5 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein CP24 10B,	-1.234
	a/b binding protein 6	chloroplatic	
Photosystem I (GO:0009522)			
Cg1g024920	Photosystem I subunit PsaN	Photosystem I reaction center subunit N,	-1.265
Cg2g020050	Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein 151,	-1.880
Cg2g021790	a/b binding protein 2 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein 13,	-1.361
Cg2g038220	a/b binding protein 3 Photosystem I subunit III	chloroplatic Photosystem I reaction center subunit III,	-1.014
Cg2g044430	Photosystem I subunit V	chloroplatic Chlorophyll a-b binding protein 3C,	-1.333
Cg2g044450	Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein 3C,	-1.625
Cg4g017260	a/b binding protein 1 Photosystem I subunit V	chloroplatic Photosystem I reaction center subunit V,	-1.799
Cg5g023620	Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein CP26,	-1.740
Cg6g006850	a/b binding protein 5 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein CP29.2,	-1.890
Cg7g006420	a/b binding protein 4 Light-harvesting complex I chlorophyll	chloroplatic Chlorophyll a-b binding protein 6A,	-1.626
Cg8g013250	a/b binding protein 1 Photosystem I subunit Psao	chloroplatic Photosystem I subunit O	-2.645
Cg9g005290	Photosystem I subunit II	Photosystem I reaction center subunit II,	-1.501
Cg9g006330	Mitochondrial pyruvate carrier 2	chloroplatic Early light-induced protein 1, chloroplatic {ECO:0000305}	1.715
Photosystem II (GO:0009523)			
Cg2g020050	Light-harvesting complex II chlorophyll	Chlorophyll a-b binding protein 151,	-1.880
Cg2g021790	a/b binding protein 2 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein 13,	-1.361
Cg2g025410	a/b binding protein 3 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein CP24 10B,	-1.234
	a/b binding protein 6	chloroplatic	



Cg2g030130			-1.401
Cg2g040770	Photosystem II oxygen-evolving enhancer protein 3	Oxygen-evolving enhancer protein 3, chloroplastic	-2.463
Cg2g044430	Light-harvesting complex II chlorophyll a/b binding protein 1	Chlorophyll a-b binding protein 3C, chloroplastic	-1.333
Cg2g044450	Light-harvesting complex II chlorophyll a/b binding protein 1	Chlorophyll a-b binding protein 3C, chloroplastic	-1.625
Cg4g018890	Mechanosensitive ion channel protein 4/5/6/7/8/9/10		-1.530
Cg5g023620	Light-harvesting complex II chlorophyll a/b binding protein 5	Chlorophyll a-b binding protein CP26, chloroplastic	-1.740
Cg6g006850	Light-harvesting complex II chlorophyll a/b binding protein 4	Chlorophyll a-b binding protein CP29.2, chloroplastic	-1.890
Cg7g005010	Photosystem II oxygen-evolving enhancer protein 2	PsbP-like protein 1, chloroplastic	-1.142
Cg7g006420	Light-harvesting complex I chlorophyll a/b binding protein 1	Chlorophyll a-b binding protein 6A, chloroplastic	-1.626
Cg7g012220	Photosystem II oxygen-evolving enhancer protein 2	Oxygen-evolving enhancer protein 2, chloroplastic	-1.749
Cg7g017970	Photosystem II PsbY protein	Photosystem II core complex proteins psbY, chloroplastic	-1.122
Cg9g006330	Mitochondrial pyruvate carrier 2	Early light-induced protein 1, chloroplastic {ECO:0000305}	1.715
Photosynthetic electron transport chain (GO:0009767)			
Cg4g017260	Photosystem I subunit V	Photosystem I reaction center subunit V, chloroplastic	-1.799
Cg5g001280	2-hydroxyacyl-CoA lyase 1 [EC:4.1.-.-]	NAD(P)H-quinone oxidoreductase subunit S, chloroplastic {ECO:0000305}	-1.221
Cg6g024950	Cell division protease FtsH [EC:3.4.24.-]	ATP-dependent zinc metalloprotease FTSH 6, chloroplastic	2.825
Cg8g013250	Photosystem I subunit PsbO	Photosystem I subunit O	-2.645
Photosystem II oxygen evolving complex (GO:0009654)			
Cg2g030130			-1.401
Cg2g040770	Photosystem II oxygen-evolving enhancer protein 3	Oxygen-evolving enhancer protein 3, chloroplastic	-2.463
Cg7g005010	Photosystem II oxygen-evolving enhancer protein 2	PsbP-like protein 1, chloroplastic	-1.142
Cg7g012220	Photosystem II oxygen-evolving enhancer protein 2	Oxygen-evolving enhancer protein 2, chloroplastic	-1.749
Photosynthesis, light reaction (GO:0019684)			
Cg2g014580	Photosystem II Psb27 protein	Photosystem II repair protein PSB27-H1, chloroplastic	-1.149
Cg2g020050	Light-harvesting complex II chlorophyll a/b binding protein 2	Chlorophyll a-b binding protein 151, chloroplastic	-1.880
Cg2g021790	Light-harvesting complex II chlorophyll a/b binding protein 3	Chlorophyll a-b binding protein 13, chloroplastic	-1.361
Cg2g025410	Light-harvesting complex II chlorophyll a/b binding protein 6	Chlorophyll a-b binding protein CP24 10B, chloroplastic	-1.234
Cg2g044430	Light-harvesting complex II chlorophyll	Chlorophyll a-b binding protein 3C, chloroplastic	-1.333

Cg2g044450	a/b binding protein 1 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein 3C,	-1.625
Cg4g017260	a/b binding protein 1 Photosystem I subunit V	chloroplatic Photosystem I reaction center subunit V,	-1.799
Cg5g001280	2-hydroxyacyl-CoA lyase 1 [EC:4.1.-.-]	chloroplatic NAD(P)H-quinone oxidoreductase subunit S,	-1.221
Cg5g023620	Light-harvesting complex II chlorophyll	chloroplatic {ECO:0000305} Chlorophyll a-b binding protein CP26,	-1.740
Cg6g006850	a/b binding protein 5 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein CP29.2,	-1.890
Cg7g006420	a/b binding protein 4 Light-harvesting complex I chlorophyll	chloroplatic Chlorophyll a-b binding protein 6A,	-1.626
Cg8g013250	a/b binding protein 1 Photosystem I subunit PsalO	chloroplatic Photosystem I subunit O	-2.645
Cg6g024950	Cell division protease FtsH [EC:3.4.24.-]	ATP-dependent zinc metalloprotease FTSH 6,	2.825
Thylakoid (GO:0009579)			
Cg1g024920	Photosystem I subunit PsaN	Photosystem I reaction center subunit N,	-1.265
Cg1g027120	Violaxanthin de-epoxidase [EC:1.23.5.1]	chloroplatic Violaxanthin de-epoxidase, chloroplatic	1.227
Cg2g001710	Enoyl-[acyl-carrier protein] reductase I	Enoyl-[acyl-carrier-protein] reductase	1.679
Cg2g014580	[EC:1.3.1.9 1.3.1.10] Photosystem II Psb27 protein	[NADH], chloroplatic Photosystem II repair protein PSB27-H1,	-1.149
Cg2g020050	Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein 151,	-1.880
Cg2g021790	a/b binding protein 2 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein 13,	-1.361
Cg2g025410	a/b binding protein 3 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein CP24 10B,	-1.234
Cg2g030130	a/b binding protein 6	chloroplatic	-1.401
Cg2g038220	Photosystem I subunit III	Photosystem I reaction center subunit III,	-1.014
Cg2g040770	Photosystem II oxygen-evolving	chloroplatic Oxygen-evolving enhancer protein 3,	-2.463
Cg2g044230	enhancer protein 3 Translation initiation factor 3 subunit D	chloroplatic Cold-regulated 413 inner membrane protein 1,	1.369
Cg2g044430	Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein 3C,	-1.333
Cg2g044450	a/b binding protein 1 Light-harvesting complex II chlorophyll	chloroplatic Chlorophyll a-b binding protein 3C,	-1.625
Cg2g044950	a/b binding protein 1 9-cis-epoxycarotenoid dioxygenase	chloroplatic 9-cis-epoxycarotenoid dioxygenase NCED1,	-3.481
Cg3g024680	[EC:1.13.11.51] Plastocyanin	chloroplatic Plastocyanin, chloroplatic	-1.448
Cg4g006740	Solute carrier family 39 (zinc	Zinc transporter 4, chloroplatic	-1.718
Cg4g017260	transporter), member 1/2/3 Photosystem I subunit V	Photosystem I reaction center subunit V,	-1.799
		chloroplatic	



Cg4g018890	Mechanosensitive ion channel protein 4/5/6/7/8/9/10		-1.530
Cg5g001280	2-hydroxyacyl-CoA lyase 1 [EC:4.1.-.-]	NAD(P)H-quinone oxidoreductase subunit S, chloroplastic {ECO:0000305}	-1.221
Cg5g009510	Magnesium dechelataase [EC:4.99.1.10]	Protein STAY-GREEN 1, chloroplastic	1.601
Cg5g018720	Arsenate reductase [EC:1.20.4.1]	Rhodanese-like domain-containing protein 14, chloroplastic	-1.171
Cg5g023620	Light-harvesting complex II chlorophyll a/b binding protein 5	Chlorophyll a-b binding protein CP26, chloroplastic	-1.740
Cg5g031990	2-methylene-furan-3-one reductase [EC:1.3.1.105]	Chloroplast envelope quinone oxidoreductase homolog {ECO:0000303 PubMed:20424175}	1.736
Cg5g038890		Nitrogen regulatory protein P-II homolog	1.759
Cg6g006850	Light-harvesting complex II chlorophyll a/b binding protein 4	Chlorophyll a-b binding protein CP29.2, chloroplastic	-1.890
Cg6g024950	Cell division protease FtsH [EC:3.4.24.-]	ATP-dependent zinc metalloprotease FTSH 6, chloroplastic	2.825
Cg7g005010	Photosystem II oxygen-evolving enhancer protein 2	PsbP-like protein 1, chloroplastic	-1.142
Cg7g006420	Light-harvesting complex I chlorophyll a/b binding protein 1	Chlorophyll a-b binding protein 6A, chloroplastic	-1.626
Cg7g012220	Photosystem II oxygen-evolving enhancer protein 2	Oxygen-evolving enhancer protein 2, chloroplastic	-1.749
Cg7g012360	Glutathione S-transferase [EC:2.5.1.18]	Glutathione S-transferase F9	-1.318
Cg7g014530	Pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	Dihydrolipoyllysine-residue acetyltransferase component 4 of pyruvate dehydrogenase complex, chloroplastic	1.067
Cg7g017970	Photosystem II PsbY protein	Photosystem II core complex proteins psbY, chloroplastic	-1.122
Cg8g000920	Signal recognition particle 43 kDa protein	Signal recognition particle 43 kDa protein, chloroplastic	-1.144
Cg8g013250	Photosystem I subunit PsbO	Photosystem I subunit O	-2.645
Cg9g005290	Photosystem I subunit II	Photosystem I reaction center subunit II, chloroplastic	-1.501
Cg9g006330	Mitochondrial pyruvate carrier 2	Early light-induced protein 1, chloroplastic {ECO:0000305}	1.715
Cg9g006690		Photosynthetic NDH subunit of subcomplex B 5, chloroplastic {ECO:0000303 PubMed:21785130}	-1.012
CgUng00263 0	ATPase family AAA domain-containing protein 2 [EC:3.6.1.-] Photosynthesis, dark reaction (GO:0019685)	Thylakoid lumenal 15.0 kDa protein 2, chloroplastic	-1.004
Cg4g021720	Ribulose-bisphosphate carboxylase small chain [EC:4.1.1.39]	Ribulose bisphosphate carboxylase small chain, chloroplastic	1.954
Cg7g006810	Transketolase [EC:2.2.1.1]	Transketolase-1, chloroplastic	4.959
Carbon fixation in photosynthetic organisms (ko00710)			
Cg5g000690	Malate dehydrogenase [EC:1.1.1.37]	Oligopeptide transporter 7	2.225
Cg9g002710	Malate dehydrogenase (decarboxylating) [EC:1.1.1.39]	F-box protein At2g17036	2.633
Cg7g006810	Transketolase [EC:2.2.1.1]	Transketolase-1, chloroplastic	4.959

Cg2g008710	Phosphoenolpyruvate carboxylase [EC:4.1.1.31]	Phosphoenolpyruvate carboxylase 2	1.414
Cg4g021720	Ribulose-bisphosphate carboxylase small chain [EC:4.1.1.39]	Ribulose bisphosphate carboxylase small chain, chloroplastic	1.954
Cg3g013480	Phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	Phosphoenolpyruvate carboxykinase (ATP)	3.955

**Table S11.** DEGs involved in carbon, carbohydrate and energy metabolisms in leaves of *C. grandis* seedlings exposed to Cu-toxicity

Accession No.	KEGG	Swiss-Prot	Log <sub>2</sub> (FC)
Carbon metabolism (ko01200)			
Cg5g000690	Malate dehydrogenase [EC:1.1.1.37]	Oligopeptide transporter 7	2.225
Cg9g002710	Malate dehydrogenase (decarboxylating) [EC:1.1.1.39]	F-box protein At2g17036	2.633
Cg5g000260	Pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic	2.284
Cg5g040000	Pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic	1.723
Cg2g044960	Pyruvate dehydrogenase E1 component beta subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic	1.708
Cg3g020270	Pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	Dihydrolipoyllysine-residue acetyltransferase component 5 of pyruvate dehydrogenase complex, chloroplastic	1.308
Cg7g014530	Pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	Dihydrolipoyllysine-residue acetyltransferase component 4 of pyruvate dehydrogenase complex, chloroplastic	1.067
Cg8g002550	Pyruvate kinase [EC:2.7.1.40]	Pyruvate kinase isozyme A, chloroplastic	1.707
Cg9g006500	Pyruvate kinase [EC:2.7.1.40]	Pyruvate kinase isozyme A, chloroplastic	1.238
Cg9g028010	Pyruvate kinase [EC:2.7.1.40]	Plastidial pyruvate kinase 2	1.374
Cg2g008710	Phosphoenolpyruvate carboxylase [EC:4.1.1.31]	Phosphoenolpyruvate carboxylase 2	1.414
Cg3g013480	Phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	Phosphoenolpyruvate carboxykinase (ATP)	3.955
Cg3g015300	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [EC:5.4.2.11]	Metal-independent phosphoserine phosphatase	1.759
Cg4g020570	Acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]	Biotin carboxylase 2, chloroplastic	2.541
Cg5g042320	Acetyl-CoA carboxylase carboxyl transferase subunit alpha [EC:6.4.1.2 2.1.3.15]		1.817
Cg6g025700	Acetyl-CoA carboxylase biotin carboxyl carrier protein	Biotin carboxyl carrier protein of acetyl-CoA carboxylase 1, chloroplastic	1.829
Cg9g001500	Dihydrolipoamide dehydrogenase [EC:1.8.1.4]	Dihydrolipoyl dehydrogenase 1, chloroplastic	1.144
Cg7g006810	Transketolase [EC:2.2.1.1]	Transketolase-1, chloroplastic	4.959
Cg2g020490	Acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	Acetyl-CoA acetyltransferase, cytosolic 1	1.243
Cg5g009780	(S)-2-hydroxy-acid oxidase [EC:1.1.3.15]	Probable transcriptional regulator SLK2	2.193
Cg5g007370	Glutamate dehydrogenase (NAD(P) <sup>+</sup> ) [EC:1.4.1.3]	Glutamate dehydrogenase 2	1.745
Cg4g021720	Ribulose-bisphosphate carboxylase small chain [EC:4.1.1.39]	Ribulose bisphosphate carboxylase small chain, chloroplastic	1.954
Cg4g004610	6-phosphofructokinase 1 [EC:2.7.1.11]	ATP-dependent 6-phosphofructokinase 3	1.958
Cg1g013660	6-phosphofructokinase 1 [EC:2.7.1.11]	ATP-dependent 6-phosphofructokinase 3	1.420
Cg7g022330	6-phosphofructokinase 1 [EC:2.7.1.11]	Acyl carrier protein 1, chloroplastic	-1.663
Cg7g016170	6-phosphogluconolactonase [EC:3.1.1.31]	Probable 6-phosphogluconolactonase 1	-1.087
Cg9g001560	Acetate/butyrate---CoA ligase [EC:6.2.1.1]	Acetate/butyrate--CoA ligase AAE7,	-1.161

Cg6g007590	6.2.1.2] S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase [EC:1.1.1.284 1.1.1.1]	peroxisomal Alcohol dehydrogenase-like 2	-2.347
Cg5g008070	3-hydroxyisobutyryl-CoA hydrolase [EC:3.1.2.4]	3-hydroxyisobutyryl-CoA hydrolase-like protein 2, mitochondrial	-1.318
Cg3g025260	Catalase [EC:1.11.1.6]	Catalase	-1.191
Starch and sucrose metabolism (ko00500)			
Cg4g018060	Sucrose synthase [EC:2.4.1.13]	Sucrose synthase	1.848
Cg9g002460	Sucrose synthase [EC:2.4.1.13]	Sucrose synthase 2	3.483
Cg4g002030	Sucrose-phosphate synthase [EC:2.4.1.14]	Probable sucrose-phosphate synthase 1	1.365
Cg3g025200	1,4-alpha-glucan branching enzyme [EC:2.4.1.18]	1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic	1.472
Cg6g016110	1,4-alpha-glucan branching enzyme [EC:2.4.1.18]	1,4-alpha-glucan-branching enzyme 1, chloroplastic/amyloplastic	1.133
Cg4g020710	Isoamylase [EC:3.2.1.68]	Isoamylase 1, chloroplastic	1.749
Cg5g008610	Trehalose 6-phosphate phosphatase [EC:3.1.3.12]	Probable trehalose-phosphate phosphatase G	1.209
Cg2g006510	Trehalose 6-phosphate phosphatase [EC:3.1.3.12]	Protein KINESIN LIGHT CHAIN-RELATED 2	-1.191
Cg4g022560	Trehalose 6-phosphate synthase/phosphatase [EC:2.4.1.15 3.1.3.12]	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 11	1.050
Cg5g004730	Trehalose 6-phosphate synthase/phosphatase [EC:2.4.1.15 3.1.3.12]	Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9	-2.681
Cg3g024770	Alpha-amylase [EC:3.2.1.1]	Probable alpha-amylase 2	1.243
Cg3g021390	Alpha-amylase [EC:3.2.1.1]	Alpha-amylase	-2.293
Cg2g017760	Beta-amylase [EC:3.2.1.2]	Beta-amylase	-1.926
Cg5g008630	Beta-fructofuranosidase [EC:3.2.1.26]	Acid beta-fructofuranosidase	3.237
Cg5g037320	Beta-glucosidase [EC:3.2.1.21]	Beta-glucosidase 11	1.166
Cg6g000800	Beta-glucosidase [EC:3.2.1.21]	Subtilisin-like protease SBT1.9	2.274
Cg8g014060	Glucan endo-1,3-beta-glucosidase 1/2/3 [EC:3.2.1.39]	Glucan endo-1,3-beta-glucosidase 14	1.055
Cg8g022430	Glucan endo-1,3-beta-glucosidase 1/2/3 [EC:3.2.1.39]	Glucan endo-1,3-beta-glucosidase	1.465
Cg9g018300	Glucan endo-1,3-beta-glucosidase 1/2/3 [EC:3.2.1.39]	Glucan endo-1,3-beta-glucosidase, basic isoform	-2.343
Cg3g023860	Endoglucanase [EC:3.2.1.4]	Endoglucanase 10	1.121
Glycolysis / gluconeogenesis (ko00010)			
Cg6g005300	Alcohol dehydrogenase (NADP <sup>+</sup> ) [EC:1.1.1.2]	NADPH-dependent aldo-keto reductase, chloroplastic	1.372
Cg7g019540	Aldehyde dehydrogenase (NAD <sup>+</sup> ) [EC:1.2.1.3]	Aldehyde dehydrogenase family 2 member B7, mitochondrial	-1.801
Cg5g032800	Alcohol dehydrogenase class-P [EC:1.1.1.1]	Alcohol dehydrogenase	-1.629
Cg5g000260	Pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic	2.284
Cg5g040000	Pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic	1.723
Cg2g044960	Pyruvate dehydrogenase E1 component	Pyruvate dehydrogenase E1 component	1.708

Cg3g020270	beta subunit [EC:1.2.4.1] Pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	subunit beta-3, chloroplastic Dihydrolipoyllysine-residue acetyltransferase component 5 of pyruvate dehydrogenase complex, chloroplastic	1.308
Cg7g014530	Pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	Dihydrolipoyllysine-residue acetyltransferase component 4 of pyruvate dehydrogenase complex, chloroplastic	1.067
Cg8g002550	Pyruvate kinase [EC:2.7.1.40]	Pyruvate kinase isozyme A, chloroplastic	1.707
Cg9g006500	Pyruvate kinase [EC:2.7.1.40]	Pyruvate kinase isozyme A, chloroplastic	1.238
Cg9g028010	Pyruvate kinase [EC:2.7.1.40]	Plastidial pyruvate kinase 2	1.374
Cg6g009400	Pyruvate decarboxylase [EC:4.1.1.1]	Pyruvate decarboxylase 1	1.236
Cg3g013480	Phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	Phosphoenolpyruvate carboxykinase (ATP)	3.955
Cg9g001500	Dihydrolipoamide dehydrogenase [EC:1.8.1.4]	Dihydrolipoyl dehydrogenase 1, chloroplastic	1.144
Cg5g041140	Glucose-6-phosphate 1-epimerase [EC:5.1.3.15]	Putative glucose-6-phosphate 1-epimerase	1.298
Cg3g015300	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [EC:5.4.2.11]	Metal-independent phosphoserine phosphatase	1.759
Cg4g004610	6-phosphofructokinase 1 [EC:2.7.1.11]	ATP-dependent 6-phosphofructokinase 3	1.958
Cg1g013660	6-phosphofructokinase 1 [EC:2.7.1.11]	ATP-dependent 6-phosphofructokinase 3	1.420
Cg7g022330	6-phosphofructokinase 1 [EC:2.7.1.11]	Acyl carrier protein 1, chloroplastic	-1.663
Cg6g018080	Aldose 1-epimerase [EC:5.1.3.3]		-3.506
Cg9g001560	Acetate/butyrate---CoA ligase [EC:6.2.1.1 6.2.1.2]	Acetate/butyrate--CoA ligase AAE7, peroxisomal	-1.161
Cg6g007590	S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase [EC:1.1.1.284 1.1.1.1]	Alcohol dehydrogenase-like 2	-2.347
Glycolytic process (GO:0006096)			
Cg2g044960	Pyruvate dehydrogenase E1 component beta subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic	1.708
Cg3g005210		Ethylene-responsive transcription factor WRI1	2.575
Cg3g020270	Pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	Dihydrolipoyllysine-residue acetyltransferase component 5 of pyruvate dehydrogenase complex, chloroplastic	1.308
Cg5g000260	Pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic	2.284
Cg5g040000	Pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic	1.723
Cg7g014530	Pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	Dihydrolipoyllysine-residue acetyltransferase component 4 of pyruvate dehydrogenase complex, chloroplastic	1.067
Cg1g013660	6-phosphofructokinase 1 [EC:2.7.1.11]	ATP-dependent 6-phosphofructokinase 3	1.420
Cg4g004610	6-phosphofructokinase 1 [EC:2.7.1.11]	ATP-dependent 6-phosphofructokinase 3	1.958
Pyruvate metabolism (ko00620)			
Cg5g000690	Malate dehydrogenase [EC:1.1.1.37]	Oligopeptide transporter 7	2.225
Cg9g002710	Malate dehydrogenase (decarboxylating) [EC:1.1.1.39]	F-box protein At2g17036	2.633
Cg5g000260	Pyruvate dehydrogenase E1 component	Pyruvate dehydrogenase E1 component	2.284

Cg5g040000	alpha subunit [EC:1.2.4.1] Pyruvate dehydrogenase E1 component	subunit alpha-3, chloroplastic Pyruvate dehydrogenase E1 component	1.723
Cg2g044960	alpha subunit [EC:1.2.4.1] Pyruvate dehydrogenase E1 component	subunit alpha-3, chloroplastic Pyruvate dehydrogenase E1 component	1.708
Cg3g020270	beta subunit [EC:1.2.4.1] Pyruvate dehydrogenase E2 component	subunit beta-3, chloroplastic Dihydrolipoyllysine-residue acetyltransferase	1.308
Cg7g014530	(dihydrolipoamide acetyltransferase) [EC:2.3.1.12] Pyruvate dehydrogenase E2 component	component 5 of pyruvate dehydrogenase complex, chloroplastic Dihydrolipoyllysine-residue acetyltransferase	1.067
Cg8g002550	(dihydrolipoamide acetyltransferase) [EC:2.3.1.12] Pyruvate kinase [EC:2.7.1.40]; Pyruvate	component 4 of pyruvate dehydrogenase complex, chloroplastic kinase isozyme A, chloroplastic	1.707
Cg9g006500	kinase isozyme A, chloroplastic Pyruvate kinase [EC:2.7.1.40]	Pyruvate kinase isozyme A, chloroplastic	1.238
Cg9g028010	Pyruvate kinase [EC:2.7.1.40]	Plastidial pyruvate kinase 2	1.374
Cg2g008710	Phosphoenolpyruvate carboxylase [EC:4.1.1.31]	Phosphoenolpyruvate carboxylase 2	1.414
Cg3g013480	Phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	Phosphoenolpyruvate carboxykinase (ATP)	3.955
Cg9g001500	Dihydrolipoamide dehydrogenase [EC:1.8.1.4]	Dihydrolipoyl dehydrogenase 1, chloroplastic	1.144
Cg2g020490	Acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	Acetyl-CoA acetyltransferase, cytosolic 1	1.243
Cg4g020570	Acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]	Biotin carboxylase 2, chloroplastic	2.541
Cg5g042320	Acetyl-CoA carboxylase carboxyl transferase subunit alpha [EC:6.4.1.2 2.1.3.15]		1.817
Cg6g025700	Acetyl-CoA carboxylase biotin carboxyl carrier protein	Biotin carboxyl carrier protein of acetyl-CoA carboxylase 1, chloroplastic	1.829
Cg9g001560	Acetate/butyrate---CoA ligase [EC:6.2.1.1 6.2.1.2]	Acetate/butyrate--CoA ligase AAE7, peroxisomal	-1.161
Cg7g019540	Aldehyde dehydrogenase (NAD <sup>+</sup> ) [EC:1.2.1.3]	Aldehyde dehydrogenase family 2 member B7, mitochondrial	-1.801
Citrate cycle (TCA cycle) (ko00020)			
Cg5g000690	Malate dehydrogenase [EC:1.1.1.37]	Oligopeptide transporter 7	2.225
Cg5g000260	Pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic	2.284
Cg5g040000	Pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic	1.723
Cg2g044960	Pyruvate dehydrogenase E1 component beta subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic	1.708
Cg9g001500	Dihydrolipoamide dehydrogenase [EC:1.8.1.4]	Dihydrolipoyl dehydrogenase 1, chloroplastic	1.144
Cg3g020270	Pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	Dihydrolipoyllysine-residue acetyltransferase component 5 of pyruvate dehydrogenase complex, chloroplastic	1.308
Cg7g014530	Pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase)	Dihydrolipoyllysine-residue acetyltransferase component 4 of pyruvate dehydrogenase	1.067



Cg3g013480	[EC:2.3.1.12] Phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	complex, chloroplastic Phosphoenolpyruvate carboxykinase (ATP)	3.955
ATP biosynthetic process (GO:0006754)			
Cg1g013660	6-phosphofructokinase 1 [EC:2.7.1.11]	ATP-dependent 6-phosphofructokinase 3	1.420
Cg2g044960	Pyruvate dehydrogenase E1 component beta subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic	1.708
Cg3g020270	Pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	Dihydrolipoyllysine-residue acetyltransferase component 5 of pyruvate dehydrogenase complex, chloroplastic	1.308
Cg4g004610	6-phosphofructokinase 1 [EC:2.7.1.11]	ATP-dependent 6-phosphofructokinase 3	1.958
Cg5g000260	Pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic	2.284
Cg5g040000	Pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic	1.723
Cg7g014530	Pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	Dihydrolipoyllysine-residue acetyltransferase component 4 of pyruvate dehydrogenase complex, chloroplastic	1.067
Cg3g005210		Ethylene-responsive transcription factor WRI1	2.575
Cg9g013190	F-type H <sup>+</sup> -transporting ATPase subunit b	Putative ATP synthase protein YMF19	-1.145
Cg1g013420	H <sup>+</sup> -transporting ATPase [EC:3.6.3.6] ATP generation from ADP (GO:0006757)	ATPase 10, plasma membrane-type	-3.022
Cg1g013660	6-phosphofructokinase 1 [EC:2.7.1.11]	ATP-dependent 6-phosphofructokinase 3	1.420
Cg2g044960	Pyruvate dehydrogenase E1 component beta subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit beta-3, chloroplastic	1.708
Cg3g020270	Pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	Dihydrolipoyllysine-residue acetyltransferase component 5 of pyruvate dehydrogenase complex, chloroplastic	1.308
Cg4g004610	6-phosphofructokinase 1 [EC:2.7.1.11]	ATP-dependent 6-phosphofructokinase 3	1.958
Cg5g000260	Pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic	2.284
Cg5g040000	Pyruvate dehydrogenase E1 component alpha subunit [EC:1.2.4.1]	Pyruvate dehydrogenase E1 component subunit alpha-3, chloroplastic	1.723
Cg7g014530	Pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]	Dihydrolipoyllysine-residue acetyltransferase component 4 of pyruvate dehydrogenase complex, chloroplastic	1.067
Cg3g005210		Ethylene-responsive transcription factor WRI1	2.575

**Table S12.** DEGs involved in photorespiration (GO:0009853), glutathione metabolism (ko00480), cell redox homeostasis (GO:0045454) and others involved in thermal dissipation and ROS scavenging in leaves of *C. grandis* seedlings exposed to Cu-toxicity

Accession No.	KEGG	Swiss-Prot	Log <sub>2</sub> (FC)
Photorespiration (GO:0009853)			
Cg4g009780	Alanine-glyoxylate transaminase / (R)-3-amino-2-methylpropionate-pyruvate transaminase [EC:2.6.1.44 2.6.1.40]	Alanine--glyoxylate aminotransferase 2 homolog 2, mitochondrial	1.357
Cg6g010200	Alanine-glyoxylate transaminase / (R)-3-amino-2-methylpropionate-pyruvate transaminase [EC:2.6.1.44 2.6.1.40]	Alanine--glyoxylate aminotransferase 2 homolog 3, mitochondrial	1.702
Cg4g021720	Ribulose-bisphosphate carboxylase small chain [EC:4.1.1.39]	Ribulose bisphosphate carboxylase small chain, chloroplastic	1.954
Glutathione metabolism (ko00480)			
Cg5g026120	Ornithine decarboxylase [EC:4.1.1.17]	Ornithine decarboxylase	-1.980
Cg6g003160	Glutathione S-transferase [EC:2.5.1.18]	Glutathione S-transferase L3	-1.072
Cg7g012360	Glutathione S-transferase [EC:2.5.1.18]	Glutathione S-transferase F9	-1.318
Cg8g023290	Glutathione S-transferase [EC:2.5.1.18]	Glutathione S-transferase U7	-1.268
Cg9g008200	Glutathione S-transferase [EC:2.5.1.18]	Probable glutathione S-transferase	-1.889
Cg9g008210	Glutathione S-transferase [EC:2.5.1.18]	Probable glutathione S-transferase	-2.100
Cg9g008220	Glutathione S-transferase [EC:2.5.1.18]	Probable glutathione S-transferase	-1.754
Cg2g030200	Glutathione S-transferase [EC:2.5.1.18]	Cyclin-P3-1	-2.011
Cg8g023310	Glutathione S-transferase [EC:2.5.1.18]	Probable glutathione S-transferase	2.050
Cg6g002810	L-ascorbate peroxidase [EC:1.11.1.11]	L-ascorbate peroxidase 2, cytosolic	1.880
Cg2g031080	Leucyl aminopeptidase [EC:3.4.11.1]		1.399
Cg5g017120	Gamma-glutamyltranspeptidase / glutathione hydrolase / leukotriene-C4 hydrolase [EC:2.3.2.2 3.4.19.13 3.4.19.14];	Glutathione hydrolase 3	1.155
Cell redox homeostasis (GO:0045454)			
Cg2g023200	Thioredoxin 1	Thioredoxin-like protein CXXS1	-2.322
Cg9g003330	Glutaredoxin 3	Monothiol glutaredoxin-S10	-5.294
Cg9g003340	Glutaredoxin 3	Monothiol glutaredoxin-S2	-2.265
Cg2g042710	Glutaredoxin 3	Glutaredoxin-C9	3.564
Cg3g022900		CBS domain-containing protein CBSX3, mitochondrial	1.571
Cg3g024580	Nucleoredoxin [EC:1.8.1.8]	Probable nucleoredoxin 2	1.855
Cg5g036730	Glutaredoxin 3	Monothiol glutaredoxin-S9	2.627
Cg9g001500	Dihydrolipoamide dehydrogenase [EC:1.8.1.4]	Dihydrolipoyl dehydrogenase 1, chloroplastic	1.144
Others			
Cg1g027120	Violaxanthin de-epoxidase [EC:1.23.5.1]	Violaxanthin de-epoxidase, chloroplastic	1.227
Cg7g011780	Superoxide dismutase, Fe-Mn family [EC:1.15.1.1]	Superoxide dismutase [Fe], chloroplastic	-2.052
Cg8g018870	Superoxide dismutase, Cu-Zn family [EC:1.15.1.1]	Superoxide dismutase [Cu-Zn], chloroplastic	1.344
Cg5g009340	Copper chaperone for superoxide dismutase	Copper chaperone for superoxide dismutase, chloroplastic/cytosolic; AtCCS	1.588
Cg3g025260	Catalase [EC:1.11.1.6]	Catalase	-1.191

Cg1g002980	Peroxidase [EC:1.11.1.7]	Peroxidase 10	5.291
Cg1g008060	Peroxidase [EC:1.11.1.7]	Peroxidase 4	1.890
Cg2g001370	Peroxidase [EC:1.11.1.7]	Peroxidase 15	-1.607
Cg2g001400	Peroxidase [EC:1.11.1.7]	Peroxidase 15	-2.280
Cg2g001440	Peroxidase [EC:1.11.1.7]	Peroxidase 15	-3.086
		{ECO:0000303 PubMed:17936696}	
Cg2g001460	Peroxidase [EC:1.11.1.7]	Peroxidase C3	-4.173
Cg3g005370	Peroxidase [EC:1.11.1.7]	Peroxidase 15	-2.085
		{ECO:0000303 PubMed:17936696}	

**Table S13.** DEGs involved in Ca homeostasis in leaves of *C. grandis* seedlings exposed to Cu-toxicity

Accession No.	KEGG	Swiss-Prot	Log <sub>2</sub> (FC)
Calcium ion transmembrane transporter activity (GO:0015085)			
Cg5g012700	Ca <sup>2+</sup> -transporting ATPase [EC:3.6.3.8]	Calcium-transporting ATPase 9, plasma membrane-type	-1.120
Cg2g020060	Ca <sup>2+</sup> -transporting ATPase [EC:3.6.3.8]	Calcium-transporting ATPase 12, plasma membrane-type	-1.457
Cg5g034830	Ca <sup>2+</sup> -transporting ATPase [EC:3.6.3.8]	Calcium-transporting ATPase 12, plasma membrane-type	-1.593
Cg3g010620	Ca <sup>2+</sup> -transporting ATPase [EC:3.6.3.8]	Calcium-transporting ATPase 12, plasma membrane-type	2.368
Cg6g003500	Ca <sup>2+</sup> -transporting ATPase [EC:3.6.3.8]	Calcium-transporting ATPase 4, endoplasmic reticulum-type	1.274
Cg3g022310	Calcium uniporter protein, mitochondrial	Calcium uniporter protein 2, mitochondrial	2.306
Cg4g022490	Glutamate receptor, ionotropic, plant	Glutamate receptor 2.8; Ligand-gated ion channel 2.8	2.004
Cg6g006900	Ca <sup>2+</sup> :H <sup>+</sup> antiporter	Vacuolar cation/proton exchanger 3; Ca(2+)/H(+) antiporter CAX3; Ca(2+)/H(+) exchanger 3; Protein CATION EXCHANGER 3;	-1.317
Cg8g024060	Ca <sup>2+</sup> :H <sup>+</sup> antiporter	Vacuolar cation/proton exchanger 3; Ca(2+)/H(+) antiporter CAX3; Ca(2+)/H(+) exchanger 3; Protein CATION EXCHANGER 3;	-1.613
Calcium-mediated signaling (GO:0019722)			
Cg4g022490	Glutamate receptor, ionotropic, plant	Glutamate receptor 2.8; Ligand-gated ion channel 2.8	2.004
Cg9g014450		Protein RALF-like 32	-1.347
Calmodulin binding (GO:0005516)			
Cg2g020060	Ca <sup>2+</sup> -transporting ATPase [EC:3.6.3.8]	Calcium-transporting ATPase 12, plasma membrane-type	-1.457
Cg3g010620	Ca <sup>2+</sup> -transporting ATPase [EC:3.6.3.8]	Calcium-transporting ATPase 12, plasma membrane-type	2.368
Cg5g012700	Ca <sup>2+</sup> -transporting ATPase [EC:3.6.3.8]	Calcium-transporting ATPase 9, plasma membrane-type	-1.120
Cg5g034830	Ca <sup>2+</sup> -transporting ATPase [EC:3.6.3.8]	Calcium-transporting ATPase 12, plasma membrane-type	-1.593
Cg2g014880	Interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]	G-type lectin S-receptor-like serine/threonine-protein kinase At4g03230	-2.095
Cg3g012090	Interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]	G-type lectin S-receptor-like serine/threonine-protein kinase B120	-3.348
Cg4g002250	Interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]	G-type lectin S-receptor-like serine/threonine-protein kinase SD2-5	-1.361
Cg8g018400	Interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]	G-type lectin S-receptor-like serine/threonine-protein kinase At4g03230	-2.581
Cg8g018410	Chitinase [EC:3.2.1.14]	G-type lectin S-receptor-like serine/threonine-protein kinase CES101	-2.087
Cg8g018470	Chitinase [EC:3.2.1.14]	G-type lectin S-receptor-like serine/threonine-	-1.937

protein kinase At1g11330			
Cg8g010170	Calcium/calmodulin-dependent protein kinase (CaM kinase) II [EC:2.7.11.17]	Phosphoenolpyruvate carboxylase kinase 1	2.727
Cg2g043490	Protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]	Calmodulin-binding receptor kinase CaMRLK {ECO:0000305}	1.303
Cg3g013020	FK506-binding protein 4/5 [EC:5.2.1.8]	Peptidyl-prolyl cis-trans isomerase FKBP62	-7.401
Cg5g006140	E1A/CREB-binding protein [EC:2.3.1.48]	BTB/POZ and TAZ domain-containing protein 2	-1.821
Cg5g018340		Protein IQ-DOMAIN 1 {ECO:0000303 PubMed:15960618}	-2.010
Cg9g027140	WW domain-containing oxidoreductase	Short-chain dehydrogenase TIC 32, chloroplastic	1.256
Cg9g029620	YTH domain-containing family protein	30-kDa cleavage and polyadenylation specificity factor 30 {ECO:0000303 PubMed:18479511}	1.074
Calmodulin-dependent protein kinase activity (GO:0004683)			
Cg8g010170	Calcium/calmodulin-dependent protein kinase (CaM kinase) II [EC:2.7.11.17]	Phosphoenolpyruvate carboxylase kinase 1	2.727
Calcium ion binding (GO:0005509)			
Cg1g003570	Calcium-binding protein CML	Probable calcium-binding protein CML41; Calmodulin-like protein 41	-2.486
Cg2g011280	Calcium-binding protein CML	Calcium-binding protein CML38; Calmodulin-like protein 38	-1.707
Cg3g017200	Calcium-binding protein CML	Probable calcium-binding protein CML44; Calmodulin-like protein 44	-1.082
Cg6g011100	Calcium-binding protein CML	Calcium-binding allergen Bet v 3; Allergen Bet v III;	-1.061
Cg3g021480	Calmodulin	Calmodulin-like protein 5	-2.843
Cg5g018200	Serine/threonine-protein phosphatase 2B regulatory subunit 1 (RefSeq) calcineurin B-like protein 7 (A)	Calcineurin B-like protein 7	-1.649
Cg2g022120	Centrin-1	Calcium-binding protein PBP1; KIC-related protein 2; PINOID-binding protein 1	-1.020
Cg1g015970	Interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]	Wall-associated receptor kinase-like 10	2.024
Cg5g026300	Interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]	Wall-associated receptor kinase 5	-3.253
Cg2g024270	Interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]	Wall-associated receptor kinase-like 2	-1.330
Cg7g005010	Photosystem II oxygen-evolving enhancer protein 2	PsbP-like protein 1, chloroplastic	-1.142
Cg7g012220	Photosystem II oxygen-evolving enhancer protein 2	Oxygen-evolving enhancer protein 2, chloroplastic	-1.749
Cg2g040770	Photosystem II oxygen-evolving enhancer protein 3	Oxygen-evolving enhancer protein 3, chloroplastic	-2.463
Cg3g021390	Alpha-amylase [EC:3.2.1.1]	Alpha-amylase	-2.293
Cg3g024770	Alpha-amylase [EC:3.2.1.1]	Probable alpha-amylase 2	1.243
Cg3g011670			1.974
Cg2g030130			-1.401
Cg3g022310	Calcium channel activity (GO:0005262)		

Cg4g022490	Calcium uniporter protein, mitochondrial	Calcium uniporter protein 2, mitochondrial	2.306
	Glutamate receptor, ionotropic, plant	Glutamate receptor 2.8; Ligand-gated ion channel 2.8	2.004



**Table S14.** DEGs involved in MAPK signaling pathway - plant (ko04016) in leaves of *C. grandis* seedlings exposed to Cu-toxicity

Accession No.	KEGG	Swiss-Prot	Log <sub>2</sub> (FC)
Cg3g014360	Calmodulin	Rhodanese-like domain-containing protein 6	1.692
Cg6g017010	Calmodulin	Rhodanese-like domain-containing protein 6	1.900
Cg3g021480	Calmodulin	Calmodulin-like protein 5	-2.843
Cg3g025260	Catalase [EC:1.11.1.6]	Catalase	-1.191
Cg2g038570	Mitogen-activated protein kinase kinase 4/5 [EC:2.7.12.2]	Protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 6	1.067
Cg9g020900	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Receptor kinase-like protein Xa21	1.870
Cg4g008420	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Leucine-rich repeat extensin-like protein 4	-1.176
Cg7g009010	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Receptor kinase-like protein Xa21	-1.796
Cg9g006130	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Leucine-rich repeat extensin-like protein 6	-2.603
Cg9g021300	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Probable LRR receptor-like serine/threonine- protein kinase At3g47570	-1.046
Cg9g021310	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Probable LRR receptor-like serine/threonine- protein kinase At3g47570	-1.066
Cg9g021330	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Probable LRR receptor-like serine/threonine- protein kinase At3g47570	-1.084
Cg9g021360	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Probable LRR receptor-like serine/threonine- protein kinase At3g47570	-1.128
Cg9g021390	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Probable LRR receptor-like serine/threonine- protein kinase At3g47570	-1.131
CgUng003130	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	LRR receptor-like serine/threonine-protein kinase EFR	-4.316
Cg1g015500	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	LRR receptor-like serine/threonine-protein kinase FLS2	-1.275
Cg1g015520	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	LRR receptor-like serine/threonine-protein kinase GSO2	-1.602
Cg1g015540	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Probable LRR receptor-like serine/threonine- protein kinase At3g47570	-2.467
Cg1g015570	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Probable LRR receptor-like serine/threonine- protein kinase At3g47570	-2.068
Cg1g015670	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Probable LRR receptor-like serine/threonine- protein kinase At3g47570	-1.948
Cg1g015690	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Receptor kinase-like protein Xa21	-1.414
Cg1g015720	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Probable LRR receptor-like serine/threonine- protein kinase At3g47570	-2.644
Cg1g020830	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Receptor like protein 8	-2.458
Cg2g023840	LRR receptor-like serine/threonine- protein kinase FLS2 [EC:2.7.11.1]	Receptor-like protein 12	-1.593
Cg3g001850	LRR receptor-like serine/threonine-	Probable LRR receptor-like serine/threonine-	-1.535

Cg6g012270	protein kinase FLS2 [EC:2.7.11.1] LRR receptor-like serine/threonine- protein kinase ERECTA [EC:2.7.11.1]	protein kinase At3g47570 DNA damage-repair/toleration protein DRT100	-1.908
Cg5g001390	Protein phosphatase 2C [EC:3.1.3.16]	Probable protein phosphatase 2C 8	3.181
Cg7g000680	Protein phosphatase 2C [EC:3.1.3.16]	Protein phosphatase 2C 37	1.252
Cg8g023080	Protein phosphatase 2C [EC:3.1.3.16]	Protein phosphatase 2C 3	2.730
Cg9g028610	Protein phosphatase 2C [EC:3.1.3.16]	Probable protein phosphatase 2C 8	1.958
CgUng003480	Protein phosphatase 2C [EC:3.1.3.16]	Protein phosphatase 2C 56	1.448
Cg1g007240	Transcription factor MYC2	Transcription factor bHLH25	8.612
Cg2g040740	Transcription factor MYC2	Transcription factor ILR3	-1.273
Cg1g008410	Pathogenesis-related protein 1	Basic form of pathogenesis-related protein 1	7.160
Cg6g009750	Abscisic acid receptor PYR/PYL family	Abscisic acid receptor PYL4	-2.059
Cg7g002520	Abscisic acid receptor PYR/PYL family	Abscisic acid receptor PYL4	-2.222
Cg9g008980	Ethylene-insensitive protein 3	Phosphate transporter PHO1	1.909
Cg4g007230	EIN3-binding F-box protein	EIN3-binding F-box protein 1	-1.226
Cg1g000850	Basic endochitinase B [EC:3.2.1.14]	Basic endochitinase	-3.753
Cg8g000790	Basic endochitinase B [EC:3.2.1.14]	Endochitinase	-4.533
Cg8g000800	Basic endochitinase B [EC:3.2.1.14]	Endochitinase	-4.480

**Table S15.** DEGs involved in plant hormone signal transduction (ko04075) in leaves of *C. grandis* seedlings exposed to Cu-toxicity

Accession No.	KEGG	Swiss-Prot	Log <sub>2</sub> (FC)
Auxin			
Cg6g006550	Auxin influx carrier (AUX1 LAX family)	Auxin transporter-like protein 2	-1.560
Cg4g002180	Auxin-responsive protein IAA	Auxin-responsive protein IAA29	3.122
Cg4g006940	Auxin-responsive protein IAA	Auxin-responsive protein IAA29	2.241
Cg4g021810	Auxin-responsive protein IAA	Auxin-responsive protein IAA33	1.792
Cg5g036600	Auxin response factor	Auxin response factor 7	9.405
CgUng005390	SAUR family protein	Auxin-responsive protein SAUR24 {ECO:0000305}	-1.813
Cytokinin			
Cg1g013900	Histidine-containing phosphotransfer protein	Histidine-containing phosphotransfer protein 4	6.555
Cg8g005300	Two-component response regulator ARR-B family	Myb family transcription factor EFM {ECO:0000303 PubMed:25132385}	-1.061
Gibberellin			
Cg2g032630	Phytochrome-interacting factor 3	Transcription factor bHLH149	1.435
Cg6g013650	Gibberellin receptor GID1 [EC:3.-.-.]	Probable carboxylesterase 15	1.352
Cg3g006980	Gibberellin receptor GID1 [EC:3.-.-.]	Probable carboxylesterase 6	2.007
Cg5g009820	DELLA protein	Scarecrow-like protein 28	2.092
Cg1g006390	DELLA protein	Scarecrow-like protein 32	4.915
Cg9g001400	DELLA protein	DELLA protein RGL2	-5.213
Cg9g001430	DELLA protein	DELLA protein RGL2	3.503
Abscisic acid			
Cg6g015730	ABA responsive element binding factor	Protein ABSCISIC ACID-INSENSITIVE 5	3.881
Cg5g001390	Protein phosphatase 2C [EC:3.1.3.16]	Probable protein phosphatase 2C 8	3.181
Cg7g000680	Protein phosphatase 2C [EC:3.1.3.16]	Protein phosphatase 2C 37	1.252
Cg8g023080	Protein phosphatase 2C [EC:3.1.3.16]	Protein phosphatase 2C 3	2.730
Cg9g028610	Protein phosphatase 2C [EC:3.1.3.16]	Probable protein phosphatase 2C 8	1.958
CgUng003480	Protein phosphatase 2C [EC:3.1.3.16]	Protein phosphatase 2C 56	1.448
Cg6g009750	Absciscic acid receptor PYR/PYL family	Absciscic acid receptor PYL4	-2.059
Cg7g002520	Absciscic acid receptor PYR/PYL family	Absciscic acid receptor PYL4	-2.222
Ethylene			
Cg2g038570	Mitogen-activated protein kinase kinase 4/5 [EC:2.7.12.2]	Protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 6	1.067
Cg9g008980	Ethylene-insensitive protein 3	Phosphate transporter PHO1	1.909
Cg4g007230	EIN3-binding F-box protein	EIN3-binding F-box protein 1	-1.226
Brassinosteroid			
Cg3g020940	Cyclin D3, plant	Cyclin-D3-1	2.052
Cg2g043490	Protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]	Calmodulin-binding receptor kinase CaMRLK {ECO:0000305}	1.303
Cg1g026820	Protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]	Protein BRASSINOSTEROID INSENSITIVE 1 {ECO:0000303 PubMed:9298904}	-1.285
Cg3g021510	BRI1 kinase inhibitor 1	BRI1 kinase inhibitor 1	-1.439
Jasmonic acid			
Cg1g007240	Transcription factor MYC2	Transcription factor bHLH25	8.612
Cg2g040740	Transcription factor MYC2	Transcription factor ILR3	-1.273

Salicylic acid			
Cg8g014140	Transcription factor TGA	Transcription factor TGA9 {ECO:0000303 PubMed:20805327}	1.538
Cg1g008410	Pathogenesis-related protein 1	Basic form of pathogenesis-related protein 1	7.160
Cg7g012290	Regulatory protein NPR1	BTB/POZ domain and ankyrin repeat-containing protein NPR2 {ECO:0000305}	-1.389
Cg7g012320	Regulatory protein NPR1	BTB/POZ domain and ankyrin repeat-containing protein NPR2 {ECO:0000305}	-2.602

**Table S16.** DEGs involved in hormone activated and/or mediated signaling pathways in leaves of *C. grandis* seedlings exposed to Cu-toxicity

Accession No.	KEGG	Swiss-Prot	Log <sub>2</sub> (FC)
Auxin-activated signaling pathway (GO:0009734)			
Cg1g000490	Uncharacterized protein	Protein PIN-LIKES 5 {ECO:0000303 PubMed:22504182}	1.367
Cg1g010480		Auxin-binding protein ABP19a	-1.866
Cg1g012930	ATP-binding cassette, subfamily B (MDR/TAP), member 1 [EC:3.6.3.44]	ABC transporter B family member 19	-2.700
Cg6g024720	ATP-binding cassette, subfamily B (MDR/TAP), member 1 [EC:3.6.3.44]	ABC transporter B family member 19	1.122
Cg1g021380		Probable N-acetyltransferase HLS1	1.638
Cg3g017880	Auxin efflux carrier family	Auxin efflux carrier component 6 {ECO:0000303 PubMed:15817418}	7.737
Cg6g017830	Auxin efflux carrier family	Probable auxin efflux carrier component 1c {ECO:0000305}	2.613
Cg3g023440	Integrin-linked kinase-associated serine/threonine phosphatase 2C [EC:3.1.3.16]	Protein WALLS ARE THIN 1	2.919
Cg4g002180	Auxin-responsive protein IAA	Auxin-responsive protein IAA29	3.122
Cg4g006940	Auxin-responsive protein IAA	Auxin-responsive protein IAA29	2.241
Cg4g021810	Auxin-responsive protein IAA	Auxin-responsive protein IAA33	1.792
Cg5g036600	Auxin response factor	Auxin response factor 7	9.405
Cg6g006550	Auxin influx carrier (AUX1 LAX family)	Auxin transporter-like protein 2	-1.560
CgUng005390	SAUR family protein	Auxin-responsive protein SAUR24 {ECO:0000305}	-1.813
Cg4g018940		Protein BIG GRAIN 1-like B {ECO:0000305}	1.824
Cg5g006140	E1A/CREB-binding protein [EC:2.3.1.48]	BTB/POZ and TAZ domain-containing protein 2	-1.821
Cg5g016500	Protein-serine/threonine kinase [EC:2.7.11.-]	Serine/threonine-protein kinase WAG1	-1.725
Cg6g009060		Auxin-induced in root cultures protein 12	-1.012
Cg7g016040		Protein BIG GRAIN 1-like E {ECO:0000305}	-2.521
Gibberellic acid mediated signaling pathway (GO:0009740)			
Cg3g022490	Beta-galactosidase [EC:3.2.1.23]	Protein indeterminate-domain 1 {ECO:0000303 PubMed:16784536}	1.026
Cg4g022720		Transcription factor IBH1-like 1 {ECO:0000303 PubMed:24505057}	-2.837
Cg7g019960	Xyloglucan glycosyltransferase 4 [EC:2.4.1.-]	Gibberellin-regulated protein 14	5.707
Cg8g005300	Two-component response regulator ARR-B family	Myb family transcription factor EFM {ECO:0000303 PubMed:25132385}	-1.061
Cg8g023080	Protein phosphatase 2C [EC:3.1.3.16]	Protein phosphatase 2C 3	2.730
Cg9g001400	DELLA protein	DELLA protein RGL2	-5.213
Cg9g001430	DELLA protein	DELLA protein RGL2	3.503
Ethylene-activated signaling pathway (GO:0009873)			
Cg1g013070	Acetylajmaline esterase [EC:3.1.1.80]	GDSL esterase/lipase 1 {ECO:0000303 PubMed:16126835}	1.365

Cg3g017880	Auxin efflux carrier family	Auxin efflux carrier component 6 {ECO:0000303 PubMed:15817418}	7.737
Cg5g001740	Pathogenesis-related genes transcriptional activator PTI6	Ethylene-responsive transcription factor CRF2	1.867
Cg1g019920	EREBP-like factor	Ethylene-responsive transcription factor ERF003	2.059
Cg3g005210		Ethylene-responsive transcription factor WRI1	2.575
Cg4g017840	EREBP-like factor	Ethylene-responsive transcription factor ERF016	1.591
Cg4g004100	EREBP-like factor	Dehydration-responsive element-binding protein 3	1.644
Cg4g015400	EREBP-like factor	Ethylene-responsive transcription factor ERF035	-1.807
Cg4g001690	EREBP-like factor	Ethylene-responsive transcription factor ERF003	-2.375
Cg5g037790	EREBP-like factor	Ethylene-responsive transcription factor RAP2-3	-3.275
Cg5g044100	EREBP-like factor	Ethylene-responsive transcription factor ERF034	-1.565
Cg5g044340	EREBP-like factor	Ethylene-responsive transcription factor 13	-1.305
Cg7g014820	RAV-like factor	AP2/ERF and B3 domain-containing transcription repressor RAV2	-2.294
Cg9g022880	EREBP-like factor	Ethylene-responsive transcription factor ERF106	-1.269
Cg4g007230	EIN3-binding F-box protein	EIN3-binding F-box protein 1	-1.226
	Brassinosteroid mediated signaling pathway (GO:0009742)		
Cg1g026820	Protein brassinosteroid insensitive 1 [EC:2.7.10.1 2.7.11.1]	Protein BRASSINOSTEROID INSENSITIVE 1 {ECO:0000303 PubMed:9298904}	-1.285
Cg1g028040	Somatic embryogenesis receptor kinase 1 [EC:2.7.10.1 2.7.11.1]	LRR receptor kinase BAK1 {ECO:0000305}	-2.102
Cg3g021510	BRI1 kinase inhibitor 1	BRI1 kinase inhibitor 1	-1.439
Cg4g022720		Transcription factor IBH1-like 1 {ECO:0000303 PubMed:24505057}	-2.837
Cg5g009820	DELLA protein	Scarecrow-like protein 28	2.092
Cg9g005160		Probable membrane-associated kinase regulator 1	1.083
Absciscic acid-activated signaling pathway (GO:0009738)			
Cg1g001510	Oomolality two-component system, sensor histidine kinase NIK1 [EC:2.7.13.3]	Histidine kinase 1	3.571
Cg1g007430	AP-1 complex subunit beta-1	Glycine-rich domain-containing protein 1 {ECO:0000303 Ref.4}	-1.659
Cg1g012650	Ras-related C3 botulinum toxin substrate 1	Ras-related C3 botulinum toxin substrate 1	2.152
Cg2g041170	Potein FLOWERING LOCUS T	Protein MOTHER of FT and TFL1	2.386
Cg3g013260	Hmeobox-leucine zipper protein	Homeobox-leucine zipper protein HAT22	-2.487
Cg3g020400	E3 ubiquitin-protein ligase RNF181 [EC:2.3.2.27]	E3 ubiquitin-protein ligase AIP2	6.069
Cg4g014320	AarF domain-containing kinase	Transcription factor SRM1 {ECO:0000305}	1.398
Cg5g006140	E1A/CREB-binding protein [EC:2.3.1.48]	BTB/POZ and TAZ domain-containing protein 2	-1.821
Cg5g035910		EID1-like F-box protein 3	2.693
Cg6g009750	Abscisic acid receptor PYR/PYL family	Abscisic acid receptor PYL4	-2.059
Cg6g015730	ABA responsive element binding factor	Protein ABSCISIC ACID-INSENSITIVE 5	3.881
Cg7g000680	Protein phosphatase 2C [EC:3.1.3.16]	Protein phosphatase 2C 37	1.252
Cg7g002520	Abscisic acid receptor PYR/PYL family	Abscisic acid receptor PYL4	-2.222



Cg8g023080	Protein phosphatase 2C [EC:3.1.3.16]	Protein phosphatase 2C 3	2.730
Cg9g026770		Low-temperature-induced 65 kDa protein	1.431
CgUng002190	AarF domain-containing kinase	Transcription factor SRM1 {ECO:0000305}	-1.326
CgUng003480	Protein phosphatase 2C [EC:3.1.3.16]	Protein phosphatase 2C 56	1.448
Salicylic acid mediated signaling pathway (GO:0009863)			
Cg2g042710	Glutaredoxin 3	Glutaredoxin-C9	3.564
Cg7g006930	(R)-mandelonitrile lyase [EC:4.1.2.10]	Salicylic acid-binding protein 2	1.429
Cg9g029620	YTH domain-containing family protein	30-kDa cleavage and polyadenylation specificity factor 30 {ECO:0000303 PubMed:18479511}	1.074
Cg8g007780	Mitochondrial chaperone BCS1	Protein HYPER-SENSITIVITY-RELATED 4	-2.370
Cytokinin-activated signaling pathway (GO:0009736)			
Cg1g013900	Histidine-containing phosphotransfer protein	Histidine-containing phosphotransfer protein 4	6.555
Cg5g001740	Pathogenesis-related genes transcriptional activator PTI6	Ethylene-responsive transcription factor CRF2	1.867
Jasmonic acid mediated signaling pathway (GO:0009867)			
Cg2g042710	Glutaredoxin 3	Glutaredoxin-C9	3.564

**Table S17.** DEGs involved in hormone metabolism in leaves of *C. grandis* seedlings exposed to Cu-toxicity

Accession No.	KEGG	Swiss-Prot	Log <sub>2</sub> (FC)
Absciscic acid metabolic process (GO:0009687)			
Cg1g001690	Cytochrome P450 family 26 subfamily A	Absciscic acid 8'-hydroxylase 1	6.219
Cg4g014320	AarF domain-containing kinase	Transcription factor SRM1 {ECO:0000305}	1.398
CgUng002190	AarF domain-containing kinase	Transcription factor SRM1 {ECO:0000305}	-1.326
Cg2g044950	9-cis-epoxycarotenoid dioxygenase [EC:1.13.11.51]	9-cis-epoxycarotenoid dioxygenase NCED1, chloroplastic	-3.481
Cg4g002980	Zeaxanthin epoxidase [EC:1.14.15.21]	Zeaxanthin epoxidase, chloroplastic	-1.171
Absciscic acid biosynthetic process (GO:0009688)			
Cg2g044950	9-cis-epoxycarotenoid dioxygenase [EC:1.13.11.51]	9-cis-epoxycarotenoid dioxygenase NCED1, chloroplastic	-3.481
Cg4g002980	Zeaxanthin epoxidase [EC:1.14.15.21]	Zeaxanthin epoxidase, chloroplastic	-1.171
CgUng002190	AarF domain-containing kinase	Transcription factor SRM1 {ECO:0000305}	-1.326
Cg4g014320	AarF domain-containing kinase	Transcription factor SRM1 {ECO:0000305}	1.398
Cytokinin metabolic process (GO:0009690)			
Cg3g023850	Uncharacterized protein	Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG7	2.170
Cg5g004060	Cytokinin dehydrogenase [EC:1.5.99.12]	Cytokinin dehydrogenase 1	1.246
Cg7g022650	Cytokinin dehydrogenase [EC:1.5.99.12]	Cytokinin dehydrogenase 6	-1.092
Cg4g018790	Cytokinin dehydrogenase [EC:1.5.99.12]	Cytokinin dehydrogenase 7	-2.115
Cytokinin biosynthetic process (GO:0009691)			
Cg3g023850	Uncharacterized protein	Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG7	2.170
Auxin metabolic process (GO:0009850)			
Cg1g003960	Indole-3-pyruvate monooxygenase [EC:1.14.13.168]	Indole-3-pyruvate monooxygenase YUCCA2	2.300
Cg2g013180	Pathogen-inducible salicylic acid glucosyltransferase [EC:2.4.1.-]	UDP-glycosyltransferase 74E2	2.959
Cg3g023440	Integrin-linked kinase-associated serine/threonine phosphatase 2C [EC:3.1.3.16]	Protein WALLS ARE THIN 1	2.919
Cg5g030310	Cytochrome P450 family 71 subfamily A	Cytochrome P450 83B1	3.608
Cg7g004010	Pheophorbide [EC:3.1.1.82]	Methylesterase 17	2.698
Cg8g024170	Phosphatidylinositol phospholipase C, delta [EC:3.1.4.11]	Phosphoinositide phospholipase C 2	2.238
Cg4g021380	Gibberellin 2-oxidase [EC:1.14.11.13]	2-oxoglutarate-dependent dioxygenase DAO	-1.022
Cg7g001270	Anthranilate synthase component I [EC:4.1.3.27]	Anthranilate synthase alpha subunit 1, chloroplastic	-1.583
Auxin biosynthetic process (GO:0009851)			
Cg1g003960	Indole-3-pyruvate monooxygenase [EC:1.14.13.168]	Indole-3-pyruvate monooxygenase YUCCA2	2.300
Cg3g023440	Integrin-linked kinase-associated serine/threonine phosphatase 2C [EC:3.1.3.16]	Protein WALLS ARE THIN 1	2.919
Cg5g030310	Cytochrome P450 family 71 subfamily A	Cytochrome P450 83B1	3.608
Cg8g024170	Phosphatidylinositol phospholipase C,	Phosphoinositide phospholipase C 2	2.238

delta [EC:3.1.4.11]			
Cg7g001270	Anthranilate synthase component I [EC:4.1.3.27]	Anthranilate synthase alpha subunit 1, chloroplastic	-1.583
Auxin transport (GO:0060918)			
Cg7g021600	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	ARF guanine-nucleotide exchange factor GNOM	1.069
Cg6g017830	Auxin efflux carrier family	Probable auxin efflux carrier component 1c {ECO:0000305}	2.613
Cg3g017880	Auxin efflux carrier family	Auxin efflux carrier component 6 {ECO:0000303 PubMed:15817418}	7.737
Cg3g023440	Integrin-linked kinase-associated serine/threonine phosphatase 2C [EC:3.1.3.16]	Protein WALLS ARE THIN 1	2.919
Cg4g018940		Protein BIG GRAIN 1-like B {ECO:0000305}	1.824
Cg4g024570	5'-AMP-activated protein kinase, catalytic alpha subunit [EC:2.7.11.11]	CBL-interacting serine/threonine-protein kinase 6	1.132
Cg6g024720	ATP-binding cassette, subfamily B (MDR/TAP), member 1 [EC:3.6.3.44]	ABC transporter B family member 19	1.122
Cg1g012930	ATP-binding cassette, subfamily B (MDR/TAP), member 1 [EC:3.6.3.44]	ABC transporter B family member 19	-2.700
Cg7g016040		Protein BIG GRAIN 1-like E {ECO:0000305}	-2.521
Cg5g016500	Protein-serine/threonine kinase [EC:2.7.11.-]	Serine/threonine-protein kinase WAG1	-1.725
Brassinosteroid biosynthetic process (GO:0016132)			
Cg1g001690	Cytochrome P450 family 26 subfamily A	Abscisic acid 8'-hydroxylase 1	6.219
Cg1g009640	3-epi-6-deoxocathasterone 23- monooxygenase [EC:1.14.13.112]	3-epi-6-deoxocathasterone 23-monooxygenase	-1.351
Cg3g021510	BRI1 kinase inhibitor 1	BRI1 kinase inhibitor 1	-1.439
Salicylic acid metabolic process (GO:0009696)			
Cg5g021790	Saccharopepsin [EC:3.4.23.25]	Aspartic proteinase CDR1	-4.185
Cg5g021820	Saccharopepsin [EC:3.4.23.25]	Aspartic proteinase CDR1	-1.398
Cg1g017890	2'-deoxymugineic-acid 2'-dioxygenase / mugineic-acid 3-dioxygenase [EC:1.14.11.24 1.14.11.25]	Protein DMR6-LIKE OXYGENASE 2 {ECO:0000303 PubMed:25376907}	8.980
Cg1g017900	2'-deoxymugineic-acid 2'-dioxygenase / mugineic-acid 3-dioxygenase [EC:1.14.11.24 1.14.11.25]	Protein DMR6-LIKE OXYGENASE 2 {ECO:0000303 PubMed:25376907}	6.975
Salicylic acid catabolic process (GO:0046244)			
Cg1g017890	2'-deoxymugineic-acid 2'-dioxygenase / mugineic-acid 3-dioxygenase [EC:1.14.11.24 1.14.11.25]	Protein DMR6-LIKE OXYGENASE 2 {ECO:0000303 PubMed:25376907}	8.980
Cg1g017900	2'-deoxymugineic-acid 2'-dioxygenase / mugineic-acid 3-dioxygenase [EC:1.14.11.24 1.14.11.25]	Protein DMR6-LIKE OXYGENASE 2 {ECO:0000303 PubMed:25376907}	6.975
Jasmonic acid metabolic process (GO:0009694)			
Cg2g037340	E3 ubiquitin-protein ligase ATL10/75/76/77/78 [EC:2.3.2.27]	RING-H2 finger protein ATL73	-2.282
Cg7g007580	OPC-8:0 CoA ligase 1 [EC:6.2.1.-]	4-coumarate--CoA ligase-like 5	5.062
Cg3g016650	Jasmonoyl-L-amino acid hydrolase	IAA-amino acid hydrolase ILR1-like 6	1.585

[EC:3.5.1.127]		{ECO:0000303 PubMed:11923288}	
Jasmonic acid biosynthetic process (GO:0009695)			
Cg2g037340	E3 ubiquitin-protein ligase ATL10/75/76/77/78 [EC:2.3.2.27]	RING-H2 finger protein ATL73	-2.282
Cg7g007580	OPC-8:0 CoA ligase 1 [EC:6.2.1.-]	4-coumarate--CoA ligase-like 5	5.062
Gibberellin biosynthetic process (GO:0009686)			
Cg2g023660	Gibberellin 2-oxidase [EC:1.14.11.13]	Gibberellin 2-beta-dioxygenase 8	3.126
Cg2g044860	Gibberellin 2-oxidase [EC:1.14.11.13]	Gibberellin 2-beta-dioxygenase	2.853

**Table S18.** Specific primer pairs used for qRT-PCR expression analysis

<b>Genes</b>	<b>Accession No.</b>	<b>Forward primers (5'→3')</b>	<b>Reverse primers (5'→3')</b>
<i>Vicilin-like seed storage protein At2g18540</i>	Cg1g003870	ACTTGACAAAGGGCTCG	CTGTGCTCGGACAAACC
<i>LanC-like protein GCL1</i>	Cg1g008400	TAGAGGAGGGATTTACGC	CCCGAGATGCTTGTTA
<i>Wall-associated receptor kinase-like 10</i>	Cg1g015970	TGGTATTAGCAGGGATT	ATGATTCCGGTGAAAGAT
<i>NAC domain-containing protein 72</i>	Cg2g021360	TTCAGCCCCAGGGATAG	CAACCTTACGACCTTCAGT
<i>Bidirectional sugar transporter SWEET16</i>	Cg2g031810	AATGCCGTAGGGTTCGT	TGTGGGCGGATCTTTCT
<i>Protein CHUP1, chloroplastic</i>	Cg2g038560	TCAAACGACTGCTACAA	ACTCTGACAACTCTGCTT
<i>Protein MOTHER of FT and TFL1</i>	Cg2g041170	TCAGAAAGCGTTGAGATTG	TCAGCAGAAGCAGAGGG
<i>Plant cysteine oxidase 1 {ECO:0000303\PubMed:24599061}</i>	Cg5g031660	TTTCTTCCTCCAACCTGC	ACTGTCGGCTATCAACTT
<i>Hypothetical protein CICLE_v10033235mg [Citrus clementina]</i>	Cg7g022450	GATTTGCGATGCTTGCT	GGTTCTTGTCACCTTTTC
<i>ATP-dependent zinc metalloprotease FTSH 6, chloroplastic</i>	Cg6g024950	AAGCAGTGATGTCGTGA	TTCCCTGTTATTCCTTATGTG
<i>Pectinesterase 3</i>	Cg1g013250	GAGTGAAATGGAAGGGAT	CAAACCAAGGGAGAATG
<i>Lectin</i>	Cg4g006720	AAAAGTGGACGAGCAAT	TCTGGCAGGTAAATGTG
<i>Probable calcium-binding protein CML41</i>	Cg1g003570	AAACTCCTCCTTGTCTGC	CTTGAAAATCCAATAAACTG
<i>LOB domain-containing protein 39</i>	Cg3g012700	CGCCCGCTCAGTCAAAT	GCAAGCACGACCTCAGTAT
<i>B-box domain protein 31 {ECO:0000303\PubMed:19920209}</i>	Cg2g041050	TGATGACGATGATGGGG	GATTCTTGCTTTGTTGAG
<i>Gamma-glutamyl peptidase 5 {ECO:0000305}</i>	Cg4g023690	TTCGGGGAAGAAGGAGA	TAAGGGCTACCGCTGAT
<i>36.4 kDa proline-rich protein</i>	Cg6g012200	GATTCTCCTCTTGAACCTGGGTA	GGGGTGGCTTGTGATGC
<i>Probable alpha-mannosidase At5g13980 {ECO:0000305}</i>	Cg7g011170	GATTCCAGTGGTCGTGA	TTACTTCCATCGTCTCC
<i>Cyclin-D3-1</i>	Cg3g020940	TCCTCCTACAGGGTGCC	TTCAATAGTTGCTTCTCATA
<i>Monothiol glutaredoxin-S2</i>	Cg9g003340	ATGGCAATGGAGCGAGTA	CACCGCCGATGAACACG
<i>Endochitinase</i>	Cg8g000800	TGAAGGCTGCCAAAGTA	ACCAAAGGCTGGAAG
<i>Actin</i>	Cg1g026080	AGAACTATGAACTGCCTGATGGC	GCTTGGAGCAAGTGCTGTGATT
<i>U4/U6 small nuclear ribonucleoprotein PRP31 (PRPF31)</i>	Cg7g019550	ACTCATGGGAACGGCTGGTGGTC	TCGGCAGGCACGCATCCTTAGAG